WHAT IS CLAIMED IS:

1. A method of qualifying a prostate cancer status in a subject comprising:

(a) measuring at least one biomarker in a sample from the subject, wherein the biomarker is selected from the group consisting of:

Marker EP1: 3448 ± 19 Da,
Marker EP2: 4036 ± 22 Da,
Marker EP3: 4361 ± 24 Da,
Marker EP4: 4413 ± 24 Da,
Marker EP5: 4639 ± 26 Da,
Marker EP6: 4749 ± 26 Da,
Marker EP7: 4827± 27 Da,
Marker EP8: 5666 ± 31 Da,
Marker EP9: 8445 ± 46 Da,
Marker EP10: 11744 ± 65 Da,
Marker EP11: 14696 ± 81 Da,
Marker EP12: 24184 ± 133 Da,
Marker EP13: 48308 ± 266 Da,
Marker EP14: 53830 ± 296 Da; and combinations thereof; and,

(b) correlating the measurement with prostate cancer status.

2. The method of claim 1, wherein the prostate cancer status is selected from the group consisting of prostate cancer (PCA), prostate intraepithelial neoplasia (PIN), and benign prostate hyperplasia (BPH).

3. The method of claim 1, wherein the sample is prostate tissue extract.

4. The method of claim 1, wherein measuring comprises determining the mass of the protein.

5. The method of claim 4, wherein the mass of the protein is determined by mass spectrometry.

6. The method of claim1, wherein the sample is selected from the group consisting of blood, serum, urine, prostatic fluid, seminal fluid, semen, and prostate tissue.

7. The method of claim 5, wherein mass spectrometry is gas phase ion spectrometry.

8. The method of claim 7, wherein gas phase ion spectrometry is laser desorption ionization mass spectrometry.

9. The method of claim 1, wherein step a) further comprises detecting the marker by immunoassay.

10. The method of claim 1, wherein
step a) further comprises:
i) fractionating the sample;
ii) binding a fraction of the sample to an adsorbent; and,
iii) comprises detecting the marker by gas phase ion spectrometry.

11. The method of claim 10, wherein the adsorbent is selected from the group consisting of a hydrophilic adsorbent, a metal chelate adsorbent, and a strong anion exchange adsorbent.

12. The method of claim 1, wherein
step a) comprises:
i) embedding a portion of a tissue specimen harvested from a patient in OCT and freezing the specimen;
ii) obtaining cryosections from the tissue specimen;
iii) obtaining cell samples from the cryosections by laser capture microdissection;
iv) mixing cell samples from step (d) with lysis buffer thereby producing cell lysates;
v) diluting and vortexing the cell lysates,
vi) centrifuging the vortexed cell lysates thereby producing a supernatant fraction;

vii) binding the supernatant fraction to an adsorbent; and,

viii) comprising detecting the marker using gas phase ion spectrometry.

13. The method of claim 12, wherein the adsorbent of step a) is selected from the group consisting of a hydrophilic adsorbent, a metal chelate adsorbent, and a strong anion exchange adsorbent.

14. The method of claim 1, wherein the sample comprises the marker EP8.

15. The method of claim 1, wherein the sample comprises the markers EP2 and EP3.

16. The method of claim 1, wherein the sample comprises the markers EP2 and EP5.

17. The method of claim 1, wherein the sample comprises the markers EP3 and EP5.

18. The method of claim 1, wherein the sample comprises the markers EP2 and EP6.

19. The method of claim 1, wherein the sample comprises the markers EP3 and EP6.

20. The method of claim 1, wherein the sample comprises the markers EP5 and EP6.

21. The method of claim 1, wherein the sample comprises the markers EP2, EP3 and EP5.

22. The method of claim 1, wherein the sample comprises the markers EP2, EP3 and EP6.

23. The method of claim 1, wherein the sample comprises the markers EP2, EP3, EP4, EP5, EP6, and EP8.

24. The method of claim 8, wherein

step b) comprises:

i) generating data for each marker with the mass spectrometer, the data comprising a mass/charge ratio and an amount determination for each ion corresponding to each marker;

ii) transforming the data into computer-readable form; and,

iii) executing an algorithm with a programmable digital computer,

wherein the algorithm determines closeness-of-fit between the computer-readable data and a data set indicating a diagnosis of PCA, PIN, BPH or a negative diagnosis.

25. A method for detecting at least one marker in a sample, the method comprising:

a) obtaining a sample comprising at least one marker, where each marker is selected from the group consisting of:

Marker EP1: 3448 ± 19 Da,

Marker EP2: 4036 ± 22 Da,

Marker EP3: 4361 ± 24 Da,

Marker EP4: 4413 ± 24 Da,

Marker EP5: 4639 ± 26 Da,

Marker EP6: 4749 ± 26 Da,

Marker EP7: 4827± 27 Da,

Marker EP8: 5666 ± 31 Da,

Marker EP9: 8445 ± 46 Da,

Marker EP10: 11744 ± 65 Da,

Marker EP11: 14696 ± 81 Da,

Marker EP12: 24184 ± 133 Da,

Marker EP13: 48308 ± 266 Da, and

Marker EP14: 53830 ± 296 Da; and,

b) detecting the marker by gas phase ion spectrometry.

26. The method of claim 25, wherein gas phase ion spectrometry is laser desorption/ionization mass spectrometry.

27. The method of claim 22, wherein the sample comprises at least two markers wherein each marker is differentially present in the sample.

28. The method of claim 26, further comprising:

c) generating data for each marker with the mass spectrometer, the data comprising a mass/charge ratio and an amount determination for each ion corresponding to each marker,

d) transforming the data into computer-readable form; and

e) executing an algorithm with a programmable digital computer wherein the algorithm detects the amount determination in the computer-readable data representing the marker and determines closeness-of-fit between the computer-readable data and a data set indicating a diagnosis of PCA, PIN, BPH or a negative diagnosis.

29. The method of claim 29, wherein the algorithm comprises an artificial intelligence program.

30. The method of claim 29, wherein the artificial intelligence program is a fuzzy logic, cluster analysis or neural network.

31. The method of claim 25, wherein step a) further comprises: fractionating the sample by size exclusion chromatography or anion exchange chromatography, and collecting a fraction that includes the marker or markers.

32. The method of claim 25, wherein step a) further comprises contacting the sample with a substrate comprising an adsorbent that retains the marker and removing unretained sample.

33. The method of claim 29, wherein the substrate is a mass spectrometer probe comprising the adsorbent on a probe surface.

34. The method of claim 29, wherein the substrate is a resin, and step a) further comprises placing the resin with the marker retained by the adsorbent on a mass spectrometer probe.

35. The method of claim 29, wherein the adsorbent is selected from the group consisting of a hydrophilic adsorbent, a strong anion exchange adsorbent and a metal chelate adsorbent.

36. The method of claim 26, wherein
step a) further comprises:
i) providing a probe adapted for use with a mass spectrometer comprising an adsorbent attached thereto;
ii) contacting the sample comprising the marker with the adsorbent.

37. The method of claim 26, wherein
step a) further comprises:
i) providing a substrate comprising an adsorbent attached thereto;
ii) contacting the sample comprising the protein with the adsorbent;
iii) placing the substrate on a probe adapted for use with a mass spectrometer.

38. The method of claim 36, wherein the adsorbent is a hydrophilic adsorbent or a metal chelate adsorbent.

39. The method of claim 37, wherein the adsorbent is a hydrophilic adsorbent comprising silicon oxide.

40. The method of claim 37, wherein the adsorbent is a metal chelate adsorbent comprising copper.

41. The method of claim 37, wherein the adsorbent comprises an antibody that specifically binds to the marker.

42. A purified marker selected from the group consisting of:
Marker EP1: 3448 ± 19 Da,
Marker EP2: 4036 ± 22 Da,
Marker EP3: 4361 ± 24 Da,

Marker EP4: 4413 ± 24 Da,
Marker EP5: 4639 ± 26 Da,
Marker EP6: 4749 ± 26 Da,
Marker EP7: 4827± 27 Da,
Marker EP8: 5666 ± 31 Da,
Marker EP9: 8445 ± 46 Da,
Marker EP10: 11744 ± 65 Da,
Marker EP11: 14696 ± 81 Da,
Marker EP12: 24184 ± 133 Da,
Marker EP13: 48308 ± 266 Da, and
Marker EP14: 53830 ± 296 Da.

43. The purified protein of claim 42, produced by a process comprising:

i) fractionating a sample comprising the marker or markers by size exclusion chromatography or anion exchange chromatography; and,

ii) collecting a fraction that includes the marker or markers.

44. The purified protein of claim 42, produced by a process comprising:

i) microdissecting a cell sample comprising the marker by laser capture microdissection, thereby producing isolated cells,

ii) lysing the isolated cells producing a cell lysate,

iii) centrifuging the cell lysate, thereby producing a cell supernatant comprising the marker,

iv) contacting the cell supernatant to an adsorbent sufficient to allow the adsorbent to bind the marker;

v) washing the adsorbent to remove unbound cell supernatant; and,

vi) eluting the marker from the adsorbent.

45. A kit comprising:

(1) an adsorbent attached to a substrate, wherein the adsorbent is suitable for retaining a marker selected from the group consisting of:

Marker EP1: 3448 ± 19 Da,
Marker EP2: 4036 ± 22 Da,

Marker EP3: 4361 ± 24 Da,
Marker EP4: 4413 ± 24 Da,
Marker EP5: 4639 ± 26 Da,
Marker EP6: 4749 ± 26 Da,
Marker EP7: 4827± 27 Da,
Marker EP8: 5666 ± 31 Da,
Marker EP9: 8445 ± 46 Da,
Marker EP10: 11744 ± 65 Da,
Marker EP11: 14696 ± 81 Da,
Marker EP12: 24184 ± 133 Da,
Marker EP13: 48308 ± 266 Da, and
Marker EP14: 53830 ± 296 Da; and

(2) instructions for using the substrate to detect the marker.

46. The kit of claim 45, wherein the instructions include methods for contacting a sample comprising the marker with the adsorbent.